



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172438

TO: Chun Crowder
Location: rem/3B59/3C70
Art Unit: 1644
Thursday, December 01, 2005

Case Serial Number: 10/822300

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:46:05 ; Search time 192 Seconds
(without alignments)
1020.640 Million cell updates/sec

Title: US-10-822-300-122XAA
Perfect score: 2372
Sequence: 1 QVQLVQSGAEVKKRQSSVKV.....LKEALNHNTQKSLSPK 446

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing filter 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	446	8	ADT51689
2	2370	99.9	446	8	ADT51687
3	2368	99.8	446	8	ADT51690
4	2366	99.7	446	8	ADT51688
5	2365	99.7	446	8	ADT51686
6	2247	94.7	465	7	ADDE4199
7	2234.5	94.2	464	8	ADDE6011
8	2233.5	94.2	652	2	AAW48650
9	2232.5	94.1	470	3	AAW90935
10	2232.5	94.1	470	5	ABW74904
11	2232	94.1	445	8	ADJ11308
12	2232	94.1	464	8	ADJ11354
13	2231.5	94.1	470	3	AAW90934
14	2231.5	94.1	470	3	ABW74903
15	2229.5	94.0	449	2	AAW43339
16	2229.5	94.0	449	2	AAW9816
17	2229.5	94.0	470	3	AAW90933
18	2229.5	94.0	470	5	ABW74902
19	2226.5	93.9	470	2	AAW93037
20	2226.5	93.9	470	3	AAW43339
21	2226.5	93.9	470	3	AAW90929
22	2226.5	93.9	470	5	ABW74944
23	2226.5	93.9	470	5	ABW74898
24	2224.5	93.8	447	8	ADT51700

25	2224.5	93.8	448	6	ABR55871	Ab-55871 Human imm
26	2224.5	93.8	448	8	ADN49728	Adn49728 Human imm
27	2224.5	93.8	448	8	ADU74404	Adu74404 Human imm
28	2223.5	93.7	449	9	ADZ80769	Adz80769 Amino aci
29	2223.5	93.7	462	9	AEBO8800	AEBO8800 Anti-NGO
30	2223.5	93.7	470	3	AAW90936	AAW90936 Humanised
31	2223.5	93.7	470	5	ABW74945	ABW74945 Humanised
32	2222.5	93.7	447	8	ADT51698	Adt51698 Humanised
33	2222	93.7	583	4	AAW83156	AAW83156 Gangliosid
34	2221.5	93.7	453	8	ADT55443	Adt55443 Anti IGE
35	2221.5	93.7	453	9	AEBS6309	AEBS6309 Anti-IGE
36	2220.5	93.6	447	8	ADT51701	Adt51701 Fencolizsu
37	2218.5	93.5	447	8	ADT51699	Adt51699 Fencolizsu
38	2217.5	93.5	447	8	ADT51697	Adt51697 Fencolizsu
39	2217	93.5	448	5	AAW49203	AAW49203 Humanised
40	2217	93.5	467	9	ADY30112	Ady30112 Human Igg
41	2216.5	93.4	451	8	ADR23350	ADR23350 Human CD7
42	2216	93.4	450	8	ADL18702	Adl18702 Protein s
43	2216	93.4	450	8	ADL18708	Adl18708 Protein s
44	2214.5	93.4	447	8	ADQ31274	Adq31274 Humanised
45	2214.5	93.4	447	8	ADQ31276	Adq31276 Humanised

ALIGNMENTS

RESULT 1	
ADT51689	
ID	ADT51689 standard; protein; 446 AA.
XX	
AC	ADT51689;
XX	
DT	13-JAN-2005 (first entry)
XX	
DE	Dacilizumab antibody gamma-1 heavy chain mutant T250Q/M428L.
XX	
KW	Humanised; antibody; immunoglobulin G; IgG; gamma-1 heavy chain;
KW	FcRn binding affinity; serum half-life; dacilizumab; fencolizumab;
KW	visilizumab; M200; cancer; inflammatory disorder; asclma;
KW	autoimmune disease; viral infection; cytostatic; antiinflammatory;
KW	antiasthmatic; immunosuppressive; virucide; mutant; mutein.
OS	Homo sapiens.
XX	
XX	Synthetic.
XX	
FT	Key
FT	Misc-difference 249
FT	Misc-difference 427
FT	/note= "Substitution of wild-type Thr to Gln"
FT	/note= "Substitution of wild-type Met to Leu"
XX	
PN	WO2004092219-A2.
XX	
PD	28-OCT-2004.
XX	
PF	09-APR-2004; 2004WO-US011213.
XX	
PR	10-APR-2003; 2003US-0462014P.
PR	03-JUN-2003; 2003US-0475762P.
PR	29-AUG-2003; 2003US-0499048P.
PR	15-OCT-2003; 2003US-00687118.
XX	
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	
PI	Hinton PR, Tsurehshita N, Tso JY, Vaequez M;
XX	
DR	WPI; 2004-758341/74.
XX	
PT	New modified antibodies of class Igg that have altered binding affinities
PT	for FcRn or altered serum half-lives, useful for diagnosing or treating
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX	
PS	Claim 16, SEQ ID NO 122; 157bp; English.

XX The present invention relates to a modified human antibody of class
CC immunoglobulin G (IgG) where at least one amino acid residue from the
CC heavy chain constant (CH) region selected from amino acid residues 250,
CC 314 and 428 is different from that present in an unmodified class IGG
CC antibody, and where the FcRn binding affinity and/or serum half-life of
CC the modified antibody is altered relative to that of the unmodified
CC antibody. The numbering of the residues in the heavy chain is that of the
CC EU index. Also disclosed are methods of modifying an antibody of class
CC IGG and producing the modified antibody cited, and a pharmaceutical
CC composition comprising the above modified immunoglobulins, proteins and
CC other bioactive molecules having altered half-lives. The unmodified or
CC naturally occurring class IGG antibody is selected from daclizumab,
CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
CC heavy chain constant region is glutamic acid or glutamine, or the amino
CC acid residue 428 from the heavy chain constant region is phenylalanine or
CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
CC constant region is glutamic acid and the amino acid residue 428 from the
CC heavy chain constant region is phenylalanine, or the amino acid residue
CC 250 from the heavy chain constant region is glutamine and the amino acid
CC residue 428 from the heavy chain constant region is phenylalanine, or the
CC amino acid residue 250 from the heavy chain constant region is glutamine
CC and the amino acid residue 428 from the heavy chain constant region is
CC leucine. The modified therapeutic antibody of class IGG has an in vivo
CC elimination half-life of at least 1.3-fold longer than that of the
CC of the invention are useful for various diagnostic and therapeutic
CC purposes, especially in the treatment of cancer, inflammatory disorders
CC (e.g. asthma), autoimmune diseases or viral infections. The present
CC sequence represents a mutated region of a humanised antibody. Note: The
CC position of the mutation is numbered according to the EU index.
XX
XX Sequence 446 AA;

Query Match 100.0%; Score 2372; DB 8; Length 446;
Best Local Similarity 99.6%; Pred. No. 1.9e-133;
Matches 444; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVKKPQSSVKVCASGYSPTSRMHWRQAPQGLGWIGYINPSTGYEY 60
DB 1 QVQLVQSGAEVKKPQSSVKVCASGYSPTSRMHWRQAPQGLGWIGYINPSTGYEY 60
QY 61 NQKFKDKATITADESTNTAYMELSLRSRSDTAVYYCARGGGVFDYWGQTLTVSSASTK 120
DB 61 NQKFKDKATITADESTNTAYMELSLRSRSDTAVYYCARGGGVFDYWGQTLTVSSASTK 120
QY 121 GPSVFPPLAPSSKTSGGTAAAGCLVDPPEPTVSVNSGALTSGVHTFPVAVLQSSGLYS 180
DB 121 GPSVFPPLAPSSKTSGGTAAAGCLVDPPEPTVSVNSGALTSGVHTFPVAVLQSSGLYS 180
QY 181 LGSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPCPAPPELLGGPSVF 240
DB 181 LGSVTVTPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPCPAPPELLGGPSVF 240
QY 241 LFPFKPKDQMIKSRTEVTCVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQYNSTYR 300
DB 241 LFPFKPKDQMIKSRTEVTCVVDVSHEDPEVKFNKYVDGVEVHNKATKPREEQYNSTYR 300
QY 301 VSVLTVLHQLDNLNGEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKN 360
DB 301 VSVLTVLHQLDNLNGEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFPYSDTAVESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQQGN 420
DB 361 QVSLTCLVKGFPYSDTAVESNGQPENNYKTPPVLDSDGSFPLYSLKLTVDKSRWQQGN 420
QY 421 VFSCSVLKEALHNHYTQKSLSLSPGK 446
DB 421 VFSCSVLKEALHNHYTQKSLSLSPGK 446

RESULT 2
ADT51687

ID XX ADT51687 standard; protein; 446 AA.
AC XX ADT51687;
DT 13-JAN-2005 (first entry)
XX Daclizumab antibody gamma-1 heavy chain mutant T250Q.
DE Humanised; antibody; immunoglobulin G; IGG; gamma-1 heavy chain;
KW FcRn binding affinity; serum half-life; daclizumab; fontolizumab;
KW visilizumab; M200; cancer; inflammatory disorder; asthma;
KW autoimmune disease; viral infection; cytostatic; antiinflammatory;
KW antiaesthetic; immunosuppressive; virucide; mutant; mutein.
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
PH Misc-difference 249 /note= "Substitution of wild-type Thr to Gln"
FT
FT
XX W02004092219-A2.
XX 28-OCT-2004.
XX 09-APR-2004; 2004WO-US011213.
XX 10-APR-2003; 2003US-0462014P.
XX 03-JUN-2003; 2003US-0475762P.
XX 29-AUG-2003; 2003US-0499048P.
XX 15-OCT-2003; 2003US-00687118.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Hinton PR, Tsurushita N, Tso JY, Vaaquez M;
XX WPI; 2004-758341/74.
XX New modified antibodies of class IGG that have altered binding affinities
XX for FcRn or altered serum half-lives, useful for diagnosing or treating
XX for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX Claim 16; SEQ ID NO 120; 157pp; English.
XX The present invention relates to a modified human antibody of class
XX immunoglobulin G (IgG) where at least one amino acid residue from the
XX heavy chain constant (CH) region selected from amino acid residues 250,
XX 314 and 428 is different from that present in an unmodified class IGG
XX antibody, and where the FcRn binding affinity and/or serum half-life of
XX the modified antibody is altered relative to that of the unmodified
XX antibody. The numbering of the residues in the heavy chain is that of the
XX EU index. Also disclosed are methods of modifying an antibody of class
XX IGG and producing the modified antibody cited, and a pharmaceutical
XX composition comprising the above modified immunoglobulins, proteins and
XX other bioactive molecules having altered half-lives. The unmodified or
XX naturally occurring class IGG antibody is selected from daclizumab,
XX fontolizumab, visilizumab and M200. The amino acid residue 250 from the
XX heavy chain constant region is glutamic acid or glutamine, or the amino
XX acid residue 428 from the heavy chain constant region is phenylalanine or
XX leucine. Alternatively, the amino acid residue 250 from the heavy chain
XX constant region is glutamic acid and the amino acid residue 428 from the
XX heavy chain constant region is phenylalanine, or the amino acid residue
XX 250 from the heavy chain constant region is glutamine and the amino acid
XX residue 428 from the heavy chain constant region is phenylalanine, or the
XX amino acid residue 250 from the heavy chain constant region is glutamine
XX and the amino acid residue 428 from the heavy chain constant region is
XX leucine. The modified therapeutic antibody of class IGG has an in vivo
XX elimination half-life of at least 1.3-fold longer than that of the
XX corresponding unmodified class IGG antibody. The composition and methods
XX of the invention are useful for various diagnostic and therapeutic
XX purposes, especially in the treatment of cancer, inflammatory disorders
XX (e.g. asthma), autoimmune diseases or viral infections. The present
XX sequence represents a mutated region of a humanised antibody. Note: The
XX sequence represents a mutated region of a humanised antibody. Note: The

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OM protein - protein search, using BW model

Run on: December 1, 2005, 07:54:27 ; Search time 45 Seconds
(without alignments)
819.408 Million cell updates/sec

Title: US-10-822-300-122XAA

Perfect score: 2372

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....LKEALHNYTKSLSPGK 446

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents, AA:*

1: /cgn2_6/prodata/1/1aa/5 COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/RE COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/BACKFILE1.pep:.*
6: /cgn2_6/prodata/1/1aa/BACKFILE1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2229.5	94.0	449	1 US-08-458-516-13	Sequence 13, Appl
2	2192.5	92.4	472	2 US-09-301-593-43	Sequence 43, Appl
3	2180.5	91.9	470	2 US-09-338-741-4	Sequence 4, Appl
4	2168	91.4	452	2 US-09-027-449-71	Sequence 71, Appl
5	2168	91.4	452	2 US-09-026-985-71	Sequence 71, Appl
6	2168	91.4	452	2 US-09-121-952A-71	Sequence 71, Appl
7	2168	91.4	452	2 US-09-334-340A-71	Sequence 71, Appl
8	2168	91.4	452	2 US-09-355-014-71	Sequence 10, Appl
9	2161.5	91.1	476	1 US-08-378-939-10	Sequence 10, Appl
10	2155	90.9	489	2 US-10-104-437-3329	Sequence 3329, Ap
11	2143	90.3	454	1 US-07-834-373C-22	Sequence 22, Appl
12	2143	90.3	454	2 US-08-437-642B-22	Sequence 22, Appl
13	2143	90.3	454	2 US-08-146-206C-22	Sequence 22, Appl
14	2143	90.3	454	2 US-09-705-686-22	Sequence 22, Appl
15	2143	90.3	454	2 US-09-705-392A-22	Sequence 22, Appl
16	2143	90.3	454	2 US-09-705-398-22	Sequence 22, Appl
17	2143	90.3	454	4 PCT-US93-07832-22	Sequence 22, Appl
18	2140	90.2	453	2 US-09-301-593-18	Sequence 18, Appl
19	2134.5	90.0	466	2 US-09-698-705-11	Sequence 11, Appl
20	2131.5	89.9	468	2 US-09-485-737B-67	Sequence 67, Appl
21	2131.5	89.9	468	2 US-10-071-485-67	Sequence 67, Appl
22	2131.5	89.9	711	2 US-09-485-737B-90	Sequence 90, Appl
23	2131.5	89.9	711	2 US-10-071-485-90	Sequence 90, Appl
24	2127.5	89.7	472	2 US-09-301-593-30	Sequence 30, Appl
25	2123	89.5	467	2 US-09-049-672A-8	Sequence 8, Appl
26	2113	89.1	449	2 US-09-679-397-2	Sequence 2, Appl
27	2113	89.1	449	2 US-09-680-148-2	Sequence 2, Appl

28	2113	89.1	449	2 US-09-104-465A-2	Sequence 2, Appl
29	2113	89.1	449	2 US-10-356-974-2	Sequence 2, Appl
30	2102.5	88.6	451	2 US-09-247-352-3	Sequence 3, Appl
31	2102.5	88.6	451	2 US-09-466-635-3	Sequence 3, Appl
32	2093.5	88.3	478	2 US-08-487-550-8	Sequence 8, Appl
33	2093.5	88.3	478	2 US-09-526-098-8	Sequence 8, Appl
34	2093.5	88.3	478	2 US-09-383-916-8	Sequence 8, Appl
35	2093.5	88.3	478	2 US-09-758-173-8	Sequence 8, Appl
36	2093.5	88.3	478	2 US-09-576-424-8	Sequence 8, Appl
37	2084.5	87.9	451	1 US-08-887-352B-18	Sequence 18, Appl
38	2084.5	87.9	451	2 US-09-109-207C-18	Sequence 18, Appl
39	2084.5	87.9	451	2 US-09-282-505-2	Sequence 2, Appl
40	2084.5	87.9	451	2 US-09-034-235-2	Sequence 2, Appl
41	2084.5	87.9	451	2 US-09-296-005-18	Sequence 18, Appl
42	2084.5	87.9	451	2 US-09-282-846-2	Sequence 2, Appl
43	2084.5	87.9	451	2 US-09-680-145-2	Sequence 2, Appl
44	2084.5	87.9	451	2 US-09-920-171-18	Sequence 18, Appl
45	2084.5	87.9	451	2 US-09-716-028-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIb/IIIa
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13
Query Match 94.0%; Score 2229.5; DB 1; Length 449;
Best Local Similarity 93.5%; Pred. No. 5e-162;
Matches 420; Conservative 10; Mismatches 16; Indels 3; Gaps 1;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVQADGQGLEWIGYINPSTGYTEY 60

Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGYFTNLYIEWVRQAPGQGLEWIGVYPCSGGTNY 60
QY 61 NQKFKDKATITADSTNTAYMELSLRSEDFAVYCAR---GGGVFDYWGQGLTVTVSSA 117
Db 61 NEKFKGRVTLTVDSSTNTAYMELSLRSEDFAVYFCARRDNGYGMFAYWGQGLTVTVSSA 120
QY 118 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 177
Db 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
QY 178 LYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 237
Db 181 LYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
QY 238 SVFLPPPKPKDOXMIKSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 297
Db 241 SVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS 300
QY 298 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 357
Db 301 TYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
QY 358 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 417
Db 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
QY 418 QGNVPFSCVLEALHNHYTQKSLSLSPGK 446
Db 421 QGNVPFSCVMEALHNHYTQKSLSLSPGK 449

RESULT 2

US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.189001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086.049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 92.4%; Score 2192.5; DB 2; Length 472;
Best Local Similarity 91.2%; Pred. No. 3.5e-159;
Matches 414; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKTSRYTFTTEYTHWVRQAPGQLEWIGGINPNP 79
QY 61 NQKFKDKATITADSTNTAYMELSLRSEDFAVYCAR-----GGGVFDYWGQGLTV 112
Db 80 NQKFKGRATLVGKASATAYMELSLRSEDFAVYCARRTAYGVDEGHANDYWGQGLTV 139
QY 113 TVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 172

Db 140 TVSS-STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198
QY 173 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPE 232
Db 199 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPE 258
QY 233 LLGGPSVFLPPPKPKDOXMIKSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 292
Db 259 LLGGPSVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 318
QY 293 EQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 352
Db 319 EQNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVYTLPP 378
QY 353 SRDELTKNQSITCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 412
Db 379 SREMTKNQSITCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 438
QY 413 KSRWQGNVPFSCVLEALHNHYTQKSLSLSPGK 446
Db 439 KSRWQGNVPFSCVMEALHNHYTQKSLSLSPGK 472

RESULT 3

US-09-238-741-4
; Sequence 4, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKI, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238,741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match 91.9%; Score 2180.5; DB 2; Length 470;
Best Local Similarity 90.7%; Pred. No. 2.9e-158;
Matches 409; Conservative 16; Mismatches 21; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYRMHWVRQAPGQLEWIGALYIPGNDTSY 79
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDFAVYCAR-----GGGVFDYWGQGLTVTVS 115
Db 80 NQKFKGRATLVADKSSSTAYMQLSLTSDSAVYICARSTYGGDWYFNWVGAGITTVTVS 139
QY 116 SASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 175
Db 140 AASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199
QY 176 SGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLG 235
Db 200 SGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLG 259
QY 236 GPSVFLPPPKPKDOXMIKSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOY 295
Db 260 GPSVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOY 319
QY 296 NSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRPQVYTLPPSRD 355

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:49:39 ; Search time 165 Seconds
(without alignments)
1129.405 Million cell updates/sec

Title: US-10-822-300-122XAA

Perfect score: 2372

Sequence: 1 OVQLVQSGAEVKKPSSSVK.....LXALHNYTKSLSPGK 446

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA_Main:*

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2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	446	US-10-822-300-122	Sequence 122, App
2	2370	99.9	446	US-10-822-300-120	Sequence 120, App
3	2368	99.8	446	US-10-822-300-123	Sequence 123, App
4	2366	99.7	446	US-10-822-300-121	Sequence 121, App
5	2365	99.7	446	US-10-822-300-119	Sequence 119, App
6	2364	99.7	446	US-10-822-300-117	Sequence 117, App
7	2332.5	94.1	470	US-10-216-484-147	Sequence 147, App
8	2332.5	94.1	470	US-10-384-933-147	Sequence 147, App
9	2331.5	94.1	470	US-10-216-484-145	Sequence 145, App
10	2331.5	94.1	470	US-10-384-933-145	Sequence 145, App
11	2329.5	94.0	470	US-10-216-484-143	Sequence 143, App
12	2329.5	94.0	470	US-10-384-933-143	Sequence 143, App
13	2326.5	93.9	470	US-10-216-484-117	Sequence 117, App
14	2326.5	93.9	470	US-10-384-933-117	Sequence 117, App
15	2324.5	93.8	448	US-10-822-300-133	Sequence 133, App
16	2324.5	93.8	448	US-10-411-037-56	Sequence 56, App1
17	2324.5	93.8	448	US-10-411-026-56	Sequence 56, App1
18	2324.5	93.8	448	US-10-410-962-56	Sequence 56, App1
19	2324.5	93.8	448	US-10-411-049-56	Sequence 56, App1
20	2324.5	93.8	448	US-10-410-930-56	Sequence 56, App1
21	2324.5	93.8	448	US-10-410-997-56	Sequence 56, App1
22	2324.5	93.8	448	US-10-411-012-56	Sequence 56, App1
23	2324.5	93.8	448	US-10-287-994-56	Sequence 56, App1
24	2324.5	93.8	448	US-10-410-913-56	Sequence 56, App1
25	2324.5	93.8	448	US-10-410-980-56	Sequence 56, App1
26	2324.5	93.8	448	US-10-410-997-56	Sequence 56, App1
27	2324.5	93.8	448	US-10-492-261-56	Sequence 56, App1

28	2223.5	93.7	470	US-10-216-484-157	Sequence 157, App
29	2223.5	93.7	470	US-10-384-933-157	Sequence 157, App
30	2223.5	93.7	447	US-10-822-300-131	Sequence 131, App
31	2221.5	93.7	453	US-10-813-483-6	Sequence 6, App1
32	2221.5	93.7	453	US-11-013-966-6	Sequence 6, App1
33	2220.5	93.6	447	US-10-822-300-134	Sequence 134, App
34	2218.5	93.5	447	US-10-822-300-132	Sequence 132, App
35	2217.5	93.5	447	US-10-822-300-130	Sequence 130, App
36	2217	93.5	448	US-10-378-567-2	Sequence 2, App1
37	2213.5	93.3	470	US-10-216-484-89	Sequence 89, App1
38	2213.5	93.3	470	US-10-384-933-89	Sequence 89, App1
39	2205	93.0	465	US-10-404-724-25	Sequence 25, App1
40	2205	93.0	465	US-10-816-276-21	Sequence 21, App1
41	2204	92.9	731	US-09-825-012-46	Sequence 46, App1
42	2204	92.9	741	US-09-825-012-55	Sequence 55, App1
43	2202	92.8	448	US-10-171-452A-48	Sequence 48, App1
44	2202	92.8	448	US-10-171-452A-60	Sequence 60, App1
45	2202	92.8	448	US-10-353-708-48	Sequence 48, App1

ALIGNMENTS

RESULT 1					
US-10-822-300-122					
; Sequence 122, Application US/10822300					
; Publication No. US20050014934A1					
; GENERAL INFORMATION:					
; APPLICANT: Hinton, et al.					
; TITLE OF INVENTION: ANTIBODIES OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF					
; FILE REFERENCE: 05882, 0039, CPUS01					
; CURRENT APPLICATION NUMBER: US/10/822,300					
; CURRENT FILING DATE: 2004-04-09					
; NUMBER OF SEQ ID NOS: 146					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 122					
; LENGTH: 446					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-822-300-122					
Query Match 100.0%; Score 2372; DB 5; Length 446;					
Best Local Similarity 99.6%; Pred. No. 9.4e-146;					
Matches 444; Conservative 2; Mismatches 0; Indels 0; Gaps 0;					
QY	1	OVQLVQSGAEVKKPSSSVKSCASGYFTFTRMHWVQADGGLEWITGYNPSGYTEY	60		
DB	1	OVQLVQSGAEVKKPSSSVKSCASGYFTFTRMHWVQADGGLEWITGYNPSGYTEY	60		
QY	61	NOKFKDXTITADESTNAYMELSLRSEDTAVVYCAAGGVFDYWGQGLVTVSSASTK	120		
DB	61	NOKFKDXTITADESTNAYMELSLRSEDTAVVYCAAGGVFDYWGQGLVTVSSASTK	120		
QY	121	GSVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNVSGALTSGVTHFPVAVLQSSGLYS	180		
DB	121	GSVPEPLAPSSKSTSGTAAIGCLVKDYFPEPVTVSNVSGALTSGVTHFPVAVLQSSGLYS	180		
QY	181	LSVTVTVSSSLGTOTYICNNHKSNTKVDKVEPKSCDTHNCPAPRELGGPSVF	240		
DB	181	LSVTVTVSSSLGTOTYICNNHKSNTKVDKVEPKSCDTHNCPAPRELGGPSVF	240		
QY	241	LFPPKPKDQXMSRTPEVTVVVDVSHDPEVKNVYDGVVHNAKTRPREOYNSTYR	300		
DB	241	LFPPKPKDQXMSRTPEVTVVVDVSHDPEVKNVYDGVVHNAKTRPREOYNSTYR	300		
QY	301	VVSVTLTVTHQMLNKEIKYKSNKALPAPLEKITSKAKGPREQVYTLPPSRDELTKN	360		
DB	301	VVSVTLTVTHQMLNKEIKYKSNKALPAPLEKITSKAKGPREQVYTLPPSRDELTKN	360		
QY	361	QVSLTCLVKGFPSPDIAYEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSMOON	420		
DB	361	QVSLTCLVKGFPSPDIAYEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSMOON	420		

NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-123

Query Match 99.8%; Score 2368; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 1.7e-145;
Matches 443; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120
Db 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120
QY 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
Db 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPELLGGPSVF 240
Db 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPELLGGPSVF 240
QY 241 LFPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYR 300
Db 241 LFPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYR 300
QY 301 VVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 360
Db 301 VVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQGN 420
Db 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQGN 420
QY 421 VFCSVLXKALHNHYTQKSLSLSPGK 446
Db 421 VFCSVLXKALHNHYTQKSLSLSPGK 446

Query Match 99.9%; Score 2370; DB 5; Length 446;

Best Local Similarity 99.3%; Pred. No. 1.3e-145; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120
Db 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120
QY 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
Db 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPELLGGPSVF 240
Db 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPELLGGPSVF 240
QY 241 LFPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYR 300
Db 241 LFPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYR 300
QY 301 VVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 360
Db 301 VVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQGN 420
Db 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRWQGN 420
QY 421 VFCSVLXKALHNHYTQKSLSLSPGK 446
Db 421 VFCSVLXKALHNHYTQKSLSLSPGK 446

RESULT 3

US-10-822-300-123
; Sequence 123, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09

Query Match 99.7%; Score 2366; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 2.3e-145;
Matches 443; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120

RESULT 4

US-10-822-300-121
; Sequence 121, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-121

Query Match 99.8%; Score 2368; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 1.7e-145;
Matches 443; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 1 QVQLVQSGAEVKKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYVCARGGVFDYWGQGLTVTVSSASTK 120

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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2005, 07:46:09 ; Search time 11 Seconds

(without alignments)
194.145 Million cell updates/sec

Title: US-10-822-300-122XAA

Perfect score: 2372

Sequence: 1 QVQLVQSGAEVKKRGSSVKV.....LKEALHNHYTKSLSLSPRK 446

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA New:

1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2127	89.7	579	US-11-174-186-41	Sequence 41, Appl
2	2111	89.0	444	US-11-172-320-6	Sequence 6, Appl
3	2093.5	88.3	478	US-11-139-459-8	Sequence 8, Appl
4	2084.5	87.9	451	US-10-923-327-11	Sequence 11, Appl
5	2079.5	87.7	451	US-10-923-327-7	Sequence 9, Appl
6	2079.5	87.7	451	US-10-923-327-9	Sequence 9, Appl
7	2008.5	84.7	476	US-11-139-459-12	Sequence 12, Appl
8	2006.5	84.6	476	US-11-139-459-4	Sequence 4, Appl
9	1986	83.7	450	US-11-025-712-12	Sequence 12, Appl
10	1931.5	81.4	470	US-11-144-248-46	Sequence 46, Appl
11	1924.5	81.1	470	US-11-144-248-49	Sequence 49, Appl
12	1922.5	81.0	470	US-11-144-248-45	Sequence 45, Appl
13	1919	80.9	473	US-11-144-248-50	Sequence 50, Appl
14	1748	73.7	330	US-11-022-289-11	Sequence 11, Appl
15	1748	73.7	330	US-11-075-351-1	Sequence 1, Appl
16	1748	73.7	551	US-11-022-289-7	Sequence 7, Appl
17	1748	73.7	551	US-11-022-289-8	Sequence 8, Appl
18	1748	73.7	557	US-11-022-289-4	Sequence 4, Appl
19	1748	73.7	557	US-11-022-289-5	Sequence 5, Appl
20	1748	73.7	557	US-11-022-289-6	Sequence 6, Appl
21	1742	73.4	330	US-11-022-289-1	Sequence 1, Appl
22	1742	73.4	548	US-11-022-289-3	Sequence 3, Appl
23	1742	73.4	557	US-11-022-289-2	Sequence 2, Appl
24	1742	73.4	564	US-11-022-289-10	Sequence 10, Appl
25	1585	66.8	326	US-11-144-248-28	Sequence 28, Appl

26	1285	54.2	452	7	US-11-016-503-6	Sequence 6, Appl
27	1285	54.2	557	7	US-11-016-503-4	Sequence 4, Appl
28	1276	53.8	462	7	US-11-016-503-8	Sequence 8, Appl
29	1276	53.8	567	7	US-11-016-503-2	Sequence 2, Appl
30	1276	53.8	567	7	US-11-016-503-10	Sequence 10, Appl
31	1263	53.2	459	6	US-10-949-720-390	Sequence 390, Appl
32	1254.5	52.9	455	7	US-11-016-503-14	Sequence 14, Appl
33	1254.5	52.9	455	7	US-11-089-803-4	Sequence 4, Appl
34	1250	52.7	771	6	US-10-949-720-389	Sequence 389, Appl
35	1241	52.3	489	6	US-10-835-475-11	Sequence 11, Appl
36	1241	52.3	514	6	US-10-835-475-2	Sequence 2, Appl
37	1233.5	52.0	531	7	US-11-008-727-18	Sequence 18, Appl
38	1228	51.8	458	7	US-11-016-503-16	Sequence 16, Appl
39	1228	51.8	458	7	US-11-089-803-6	Sequence 6, Appl
40	1226.5	51.7	696	7	US-11-029-003-8	Sequence 8, Appl
41	1223	51.6	458	7	US-11-016-503-12	Sequence 12, Appl
42	1223	51.6	458	7	US-11-089-803-2	Sequence 2, Appl
43	1220	51.4	232	6	US-10-636-320-4	Sequence 4, Appl
44	1217.5	51.3	256	7	US-11-029-003-14	Sequence 14, Appl
45	1216.5	51.3	415	7	US-11-029-003-12	Sequence 12, Appl

ALIGNMENTS

```
RESULT 1
US-11-174-186-41
; Sequence 41, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Galliers, Stephen
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: heavy chain-IL2
US-11-174-186-41

Query Match      89.7%; Score 2127; DB 7; Length 579;
Best Local Similarity 88.1%; Pred. No. 4.6e-131;
Matches 393; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKRGSSVKVSCKASGYTFTSRMHVRAQAPQGLEIMGYINPSTGYEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKKRGSSVKVSCKASGYTFTSRMHVRAQAPQGLEIMGYINPSTGYEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKDKATITDESTNTAYMELSLRSEDLTAVVYCARGGVFDWGQGLTLTVSSASTX 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADDPKRPAFSLSTSTSTFTFLQINLRSEDLTAVVYCARGGVFDWGQGLTLTVSSASTX 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 GSVFPEPLADSSKSTSGGTAALGCLVVDYFPEPVTVSNMNGALTSGVHTFPAVLQSSGLYS 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GSVFPEPLADSSKSTSGGTAALGCLVVDYFPEPVTVSNMNGALTSGVHTFPAVLQSSGLYS 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LSSVTVPESSISGCTQTYICNVNHRKPSNTVDKQVPEKSDKHTHTPCGAPBLGGPSVF 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LSSVTVPESSISGCTQTYICNVNHRKPSNTVDKQVPEKSDKHTHTPCGAPBLGGPSVF 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 LFPPEKDDKMSIRPEVTCVVVDVSHEDPEVKFMWYDGVVHNAAKTPRREOYNSTR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LFPPEKDDKMSIRPEVTCVVVDVSHEDPEVKFMWYDGVVHNAAKTPRREOYNSTR 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```


QY 301 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKN 360
DB 301 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSKLTVDKSRWQGN 420
DB 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSKLTVDKSRWQGN 420
QY 421 VFSCSVLKEALHNHYTKSLSPGK 446
DB 421 VFSCSVLKEALHNHYTKSLSPGK 446

RESULT 2
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

Query Match 89.0%; Score 2111; DB 7; Length 444;
Best Local Similarity 88.1%; Pred. No. 3.8e-130;
Matches 393; Conservative 24; Mismatches 27; Indels 2; Gaps 1;

QY 1' QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
DB 1' EVQLVESGGGLVQPGGSLRLSCAASGFTSSYDMSNWVRQAPGKGLIEWVSTISSGGSVYY 60
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDVAVYCARGGVFDYWGOGTLVTVSSASTK 120
DB 61 LDSIKGRFTISRDNAKNSLYLQMNSLRADAVYCARQG--LDYWGRTLTVTVSSASTK 118
QY 121 GPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYS 180
DB 119 GPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSSGLYS 178
QY 181 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVF 240
DB 179 LSSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVF 238
QY 241 LPPPKPKDQXMTSRPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
DB 239 LPPPKPKDQXMTSRPTEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 298
QY 301 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKN 360
DB 299 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKN 358
QY 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSKLTVDKSRWQGN 420

DB 359 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSKLTVDKSRWQGN 418
QY 421 VFSCSVLKEALHNHYTKSLSPGK 446
DB 419 VFSCSVLKEALHNHYTKSLSPGK 444

RESULT 3
US-11-139-499-8
; Sequence 8, Application US/11139499
; Publication No. US20050260205A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-8

Query Match 88.3%; Score 2093.5; DB 7; Length 478;
Best Local Similarity 85.4%; Pred. No. 5.5e-129;
Matches 392; Conservative 27; Mismatches 27; Indels 13; Gaps 3;

QY 1 QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYI--NPSTGYT 58
DB 20 EVQLVESGGGLVQPGGSLRVCAVSGFTFSDHYMYWFRQAPGKPEWVGFINRKNPGGTT 79
QY 59 EYNQKFKDKATITADESTNTAYMELSLRSEDVAVYIC-----ARG----GGVFDYWG 107
DB 80 EYAAVKDRTISRDNSKSIQVLSLKLIEDTAVYICTTSVISHCRGGVCGYGFYFVG 139
QY 108 QGTLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVH 167
DB 140 QGALVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVH 199
QY 168 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPP 227
DB 200 TFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPP 259
QY 228 CPAPPELLGGPSVFLPPKPKDQXMTSRPTEVTCVVDVSHEDPEVKFNWYVDGVEVHN 287
DB 260 CPAPPELLGGPSVFLPPKPKDQXMTSRPTEVTCVVDVSHEDPEVKFNWYVDGVEVHN 319
QY 288 TKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOV 347
DB 320 TKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOV 379
QY 348 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTPPVLDSDGSPFLYS 407
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTPPVLDSDGSPFLYS 439
QY 408 KLTVDKSRWQGNVFSCSVLKEALHNHYTKSLSPGK 446
DB 440 KLTVDKSRWQGNVFSCSVLKEALHNHYTKSLSPGK 478

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:46:08 ; Search time 229 Seconds
(without alignments)
1374.086 Million cell updates/sec

Title: US-10-822-300-122XAA
Perfect score: 2372
Sequence: 1 QV0LV0SGAEVKKKPGSSVKV.....LKEALHNHYTQKSLSPGK 446

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2152	90.7	469	Q7Z7P5_HUMAN	Q7Z7P5 homo sapien
2	2138.5	90.2	480	Q6PUF1_HUMAN	Q6PUF1 homo sapien
3	2124	89.5	475	Q6N095_HUMAN	Q6N095 homo sapien
4	2117	89.2	469	Q569R4_HUMAN	Q569R4 homo sapien
5	2083.5	87.8	466	Q6N096_HUMAN	Q6N096 homo sapien
6	2081.5	87.8	470	Q6N094_HUMAN	Q6N094 homo sapien
7	2081.5	87.8	480	Q6N094_HUMAN	Q6N094 homo sapien
8	2076.5	87.5	472	Q6N089_HUMAN	Q6N089 homo sapien
9	2076	87.5	475	Q5EFES_HUMAN	Q5EFES homo sapien
10	2074	87.4	473	Q6MZV7_HUMAN	Q6MZV7 homo sapien
11	2074	87.4	475	Q6MZD6_HUMAN	Q6MZD6 homo sapien
12	2071.5	87.3	466	Q6N096_HUMAN	Q6N096 homo sapien
13	2055	86.6	544	Q6PJ95_HUMAN	Q6PJ95 homo sapien
14	2053.5	86.6	470	Q7Z5W1_HUMAN	Q7Z5W1 homo sapien
15	2049.5	86.4	478	Q6P181_HUMAN	Q6P181 homo sapien
16	2047	86.3	473	Q6P055_HUMAN	Q6P055 homo sapien
17	2047	86.3	475	Q6GMW7_HUMAN	Q6GMW7 homo sapien
18	2045.5	86.2	518	Q6N030_HUMAN	Q6N030 homo sapien
19	2043	86.1	465	Q6GMK6_HUMAN	Q6GMK6 homo sapien
20	2034	85.8	475	Q5RE17_PONPY	Q5RE17 pongo pygma
21	2023.5	85.3	476	Q6GMK1_HUMAN	Q6GMK1 homo sapien
22	2023	85.3	481	Q6N097_HUMAN	Q6N097 homo sapien
23	2022	85.2	519	Q5EBN2_HUMAN	Q5EBN2 homo sapien
24	2019.5	85.1	482	Q7Z3J1_HUMAN	Q7Z3J1 homo sapien
25	1919.5	80.9	464	Q6MZU6_HUMAN	Q6MZU6 homo sapien
26	1899	80.1	465	Q6PEC4_HUMAN	Q6PEC4 homo sapien
27	1897	80.0	521	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
28	1885.5	79.5	470	Q6NCN4_HUMAN	Q6NCN4 homo sapien
29	1843.5	77.7	417	Q6N093_HUMAN	Q6N093 homo sapien
30	1820.5	76.7	473	Q8TC63_HUMAN	Q8TC63 homo sapien
31	1797	75.8	348	Q6PYX1_HUMAN	Q6PYX1 homo sapien

32	1796	75.7	476	Q6MZX7_HUMAN	Q6MZX7 homo sapien
33	1748	73.7	330	IGHG1_HUMAN	IGHG1 homo sapien
34	1603	67.6	487	Q65ZL2_SMURI	Q65ZL2 mus sp. fv/
35	1597.5	67.3	509	Q8NF17_HUMAN	Q8NF17 homo sapien
36	1595	66.8	326	IGHG2_HUMAN	IGHG2 homo sapien
37	1574	66.4	465	Q6PUB2_MOUSE	Q6PUB2 mus musculu
38	1571.5	66.3	327	IGHG4_HUMAN	IGHG4 homo sapien
39	1571	66.2	473	Q9DBL4_MOUSE	Q9DBL4 mus musculu
40	1560.5	65.8	468	Q569W9_MOUSE	Q569W9 mus musculu
41	1557.5	65.7	470	Q7WTK1_MOUSE	Q7WTK1 mus musculu
42	1554	65.5	463	Q99LC4_MOUSE	Q99LC4 mus musculu
43	1544.5	65.1	458	Q5BJZ2_RAT	Q5BJZ2 rattus norv
44	1529.5	64.5	472	Q6PJ47_MOUSE	Q6PJ47 mus musculu
45	1527.5	64.4	468	Q505N9_MOUSE	Q505N9 mus musculu

ALIGNMENTS

RESULT 1
Q7Z7P5_HUMAN PRELIMINARY; PRT; 469 AA.
ID Q7Z7P5_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tshibuyi S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
NIH MGC Project;
SUBMITTED (Apr-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC051328; AAH51328.1; -, mRNA.
DR HSSP: P01857; IGH1.
DR SMR: Q7Z7P5; 20-469.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-sect; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.

KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5B812BAAF795C CRC64;
Query Match 90.7%; Score 2152; DB 2; Length 469;
Best Local Similarity 90.0%; Pred. No. 2.1e-135;
Matches 405; Conservative 19; Mismatches 22; Indels 4; Gaps 2;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGVTEY 60
DB 20 QVHLVQSGAEVKKPGASVKLSCKTSQYNFSSYDLIWRQAPGQGLEWGWISAHNGDTKY 79
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYCA---RGG-GVDFYWGQGLTVTVSS 116
DB 80 ARKFGQGRVTMTDTTSATTSYMEFRSLRSDTALFYCATKSRQGVGDFDSWGQGLTVTVSS 139
QY 117 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176
DB 140 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 199
QY 177 GLYSLSVVTVTPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 236
DB 200 GLYSLSVVTVTPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 259
QY 237 PSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296
DB 260 PSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319
QY 297 STYRVSVLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
DB 320 STYRVSVLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 379
QY 357 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFLYSLKLTVDKSRW 416
DB 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFLYSLKLTVDKSRW 439
QY 417 QGNGVFCSVLXALHNHYTQKSLSLSPGK 446
DB 440 QGNGVFCSVLXALHNHYTQKSLSLSPGK 469
RESULT 2
Q6PJF1 HUMAN
ID Q6PJF1 HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6PJF1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2].
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC016381; AAH16381.1; -; mRNA.
RL HSP; P01861; IADO
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;
Query Match 90.2%; Score 2138.5; DB 2; Length 480;
Best Local Similarity 88.1%; Pred. No. 1.7e-134;
Matches 406; Conservative 18; Mismatches 22; Indels 15; Gaps 1;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGVTEY 60
DB 20 QVQLVQSGAEVKKPGSSVKVSCKASGSGSFVISWRQAPGQGLAWGGIIIPAFDITKY 79
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYCARGGGVF-----DY 105
DB 80 AQNFQDRTVTSADESDTAYMELSLRSEDYATYYCARDLALYELWSGPHTDKYYGLDV 139
QY 106 WGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSG 165
DB 140 WGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSG 199
QY 166 VHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTC 225
DB 200 VHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHKPSNTKVDKVEPKSCDKTHTC 259
QY 226 PPCPAPELLGGPSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 285
DB 260 PPCPAPELLGGPSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319
QY 286 AKTKPREEQNSTYRVSVLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREP 345
DB 320 AKTKPREEQNSTYRVSVLVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREP 379
QY 346 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFFL 405
DB 380 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGSGFFL 439
QY 406 YSKLTVDKSRWQNGVFCSVLXALHNHYTQKSLSLSPGK 446
DB 440 YSKLTVDKSRWQNGVFCSVLXALHNHYTQKSLSLSPGK 480
RESULT 3
Q6N095 HUMAN
ID Q6N095 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6N095;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686K03196.
GN Name=DKFZp686K03196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;